

10/501127

Sequence 2002-032 US
SEQUENCE LISTING

<110> ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
<120> Paramycobacterial diagnostics and vaccines
<130> 2002-032-US
<160> 22
<170> PatentIn version 3.2
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<211> 1175
<212> DNA
<213> mycobacterium avium paratuberculosis

<220>
<221> CDS
<222> (134)..(1144)

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agaggagact tcc gtg ccg aac cga cgc cga cgc aag ctt tcg aca gcc 169
Val Pro Asn Arg Arg Arg Arg Lys Leu Ser Thr Ala
1 5 10
atg agc gcg gtc gcc gcc ctg gca gtg gcg agt cct tgc gca tac ttc 217
Met Ser Ala Val Ala Ala Leu Ala Val Ala Ser Pro Cys Ala Tyr Phe
15 20 25
ctt gtc tac gaa tcg acg gcc ggc aac aag gcg ccc gag cac cac gag 265
Leu Val Tyr Glu Ser Thr Ala Gly Asn Lys Ala Pro Glu His His Glu
30 35 40
ttc aag cag gcc gca gtg atg agc gat ctg ccg ggc gag ctg atg ggt 313
Phe Lys Gln Ala Ala Val Met Ser Asp Leu Pro Gly Glu Leu Met Gly
45 50 55 60
gcg ctg tcg cag ggc ctg tcg cag ttt ggg atc aac ctg ccc ccg gtg 361
Ala Leu Ser Gln Gly Leu Ser Gln Phe Gly Ile Asn Leu Pro Pro Val
65 70 75
ccc gcc ctg agc ggc ggc gcc acc agc act ccc ggt ctg gcc agc ccc 409
Pro Ala Leu Ser Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro
80 85 90
ggc ctg ggt agc ccc ggc ctg ggc acg ccc ggc ctg gga acg ccg ggc 457
Gly Leu Gly Ser Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly
95 100 105
ctg acc aat ccc ggt ctg acg agc ccc ggt gcg acc agt ccc ggc ctg 505
Leu Thr Asn Pro Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu
110 115 120
acc agt ccc ggc ctg acc agt cct ggt ttg acc agc ccc ggt ctg acc 553
Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr
125 130 135 140

Sequence 2002-032 US

agc ccg ggt gcg gcg ccg acg acg ccc ggg ctc acc gcg ccc ggc gcg Ser Pro Gly Ala Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala 145 150 155	601
ctg ccg acc acg ccg ggc ggc ggg gtc gcc acc ccc ggc gcc ggg ctc Leu Pro Thr Thr Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu 160 165 170	649
aac ccc gcg ctg tcc aac ccc ggg ctg acc agc ccg gcc ggg acg gcg Asn Pro Ala Leu Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala 175 180 185	697
ccg ggg ctg ggc agc ccg acc gtg gcg ccg agt gag gtg ccg atc gac Pro Gly Leu Gly Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp 190 195 200	745
tcc ggg gcc ggc ctg gac ccg ggc gcc ggt ggc acg tac ccg atc ctg Ser Gly Ala Gly Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu 205 210 215 220	793
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aac gac gtg atg caa gcc gcc aac cag ctc ggc gcg ggt cag gcg atc Asn Asp Val Met Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile 255 260 265	937
gac ctg ctc aag ggc ctg gtg atg ccg gcg atc acg cag ggc atg cac Asp Leu Leu Lys Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His 270 275 280	985
ggc ggc gcg gcc gcg ggt gct ttg ccc ggc gcg gcc ggt gct ctg ccc Gly Gly Ala Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro 285 290 295 300	1033
ggc gcg gcc ggc gcc ctg ccc ggt gcg gcc ggc gcc ctg ccg ggt gcg Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala 305 310 315	1081
gcg ggc gcc gcg ggt gcg ttg ccg gcg gcc gcc ggc gcc gcg ccg gca Ala Gly Ala Ala Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala 320 325 330	1129
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 <213> mycobacterium avium paratuberculosis
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Sequence 2002-032 US

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20 25 30

Ser Thr Ala Gly Asn Lys Ala Pro Glu His His Glu Phe Lys Gln Ala
35 40 45

Ala Val Met Ser Asp Leu Pro Gly Glu Leu Met Gly Ala Leu Ser Gln
50 55 60

Gly Leu Ser Gln Phe Gly Ile Asn Leu Pro Pro Val Pro Ala Leu Ser
65 70 75 80

Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro Gly Leu Gly Ser
85 90 95

Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly Leu Thr Asn Pro
100 105 110

Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu Thr Ser Pro Gly
115 120 125

Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Ala
130 135 140

Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala Leu Pro Thr Thr
145 150 155 160

Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu Asn Pro Ala Leu
165 170 175

Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala Pro Gly Leu Gly
180 185 190

Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp Ser Gly Ala Gly
195 200 205

Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu Gly Asp Pro Ser
210 215 220

Thr Phe Gly Asn Ala Ser Pro Ile Gly Gly Gly Gly Thr Gly Leu Gly
225 230 235 240

Gly Gly Ser Ser Ser Gly Gly Ser Gly Gly Leu Val Asn Asp Val Met
245 250 255

Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile Asp Leu Leu Lys
260 265 270

Sequence 2002-032 us

Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His Gly Gly Ala Ala
275 280 285

Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly
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Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Ala
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Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala Leu Pro Pro Val
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Met Ser Arg Leu Ser Phe Val Cys Arg Leu Leu Ala Ala Thr
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gct ttc gcc gtc gcc ctg cta ctc ggg ctg ggc gac gtg ccg cgc gcg 156
Ala Phe Ala Val Ala Leu Leu Leu Gly Leu Gly Asp Val Pro Arg Ala
15 20 25 30
gcg gcc acc gac gac cgc ctg caa ttc acc gcg acc acg ctc agc ggc 204
Ala Ala Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly
35 40 45
gcg ccg ttc aac ggc gcc agt ctg cag ggc aag ccc gcc gtg ctg tgg 252
Ala Pro Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp
50 55 60
ttc tgg acg ccg tgg tgc ccg tac tgc aac gcc gag gcc ccg ggc gtg 300
Phe Trp Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val
65 70 75
agc cgg gtg gcc gcc gcc aac ccg ggc gtc acc ttc gtc ggc gtc gcc 348
Ser Arg Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala
80 85 90
gcc cac tcc gaa gtc ggc gcc atg gcc aac ttc gtc tcc aag tac aac 396
Ala His Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn
95 100 105 110
ctg aac ttc acc acg ctc aac gac gcc gac ggc gcg atc tgg gcc cgc 444
Leu Asn Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg
115 120 125

Sequence 2002-032 US

tac ggc gtg ccc tgg cag ccc gcg tac gtg ttc tac cgg gcg gac ggc	492
Tyr Gly Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly	
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Ser Ser Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu	
145 150 155	
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 <213> mycobacterium avium paratuberculosis

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 20 25 30

Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly Ala Pro
 35 40 45

Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp Phe Trp
 50 55 60

Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val Ser Arg
 65 70 75 80

Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala Ala His
 85 90 95

Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn Leu Asn
 100 105 110

Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg Tyr Gly
 115 120 125

Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly Ser Ser
 130 135 140

Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu Leu Ala
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Ala Arg Val Ala Ala Leu Arg

[illegible]

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          20         25         30
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Ala Ile Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Ile Ala Ala Leu
Page 6

Sequence 2002-032 US

35

40

45

Asn Ala Ser Asp Pro Ala Ala Ala Gln Gln Leu Asn Ser Ser Pro Met
 50 55 60

Ala Gln Ser Tyr Ile Gln Arg Phe Leu Ala Ser Pro Pro Ala Lys Arg
 65 70 75 80

Gln Gln Met Ala Gln Gln Ile Gln Gly Met Pro Ala Ala Gln Gln Tyr
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Ile Asn Asp Ile Asn Gln Val Ala Val Thr Cys Asn Asn Phe
 100 105 110

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 Val Ser Ser Asp Leu Phe Ser Gln Ile Val Asn Ser Gly Pro Gly Ser
 5 10 15 20

ttt ctc gcc aag cag ctc ggc gtc ccg caa ccc gag acg ctg cgc cgc 153
 Phe Leu Ala Lys Gln Leu Gly Val Pro Gln Pro Glu Thr Leu Arg Arg
 25 30 35

tac cgg ccc ggt gac ccg ccg ctg gcc ggg tcg ctg ctg atc ggc ggc 201
 Tyr Arg Pro Gly Asp Pro Pro Leu Ala Gly Ser Leu Leu Ile Gly Gly
 40 45 50

gag ggc cgc gtg gtc gag ccg ctg cgg gcg gcg ctg gcc aag gac tac 249
 Glu Gly Arg Val Val Glu Pro Leu Arg Ala Ala Leu Ala Lys Asp Tyr
 55 60 65

gac ctg gtc ggc aac aac ctg ggc ggg cgc tgg gcc gac cgg ttc ggc 297
 Asp Leu Val Gly Asn Asn Leu Gly Gly Arg Trp Ala Asp Arg Phe Gly
 70 75 80

ggg ctg gtc ttc gac gcc acc ggg atc acc acc ccg gag ggc ctg aag 345
 Gly Leu Val Phe Asp Ala Thr Gly Ile Thr Thr Pro Glu Gly Leu Lys
 85 90 95 100

ggg ctg tac gag ttc ttc acc cca ctg ctg cgc aac ctg ggt cac tgc 393
 Gly Leu Tyr Glu Phe Phe Thr Pro Leu Leu Arg Asn Leu Gly His Cys
 105 110 115

gcc cgc gtg gtg gtg gtc ggc acc acg ccc gac gcc gcc gcc ggc ccg 441
 Page 7

Sequence 2002-032 US															
Ala	Arg	Val	Val	Val	Val	Gly	Thr	Thr	Pro	Asp	Ala	Ala	Ala	Gly	Pro
			120					125					130		
cac	gag	cgg	atc	gcc	cag	cgc	gcc	ctg	gag	ggc	ttc	acc	cgg	tca	ttg
His	Glu	Arg	Ile	Ala	Gln	Arg	Ala	Leu	Glu	Gly	Phe	Thr	Arg	Ser	Leu
		135					140					145			
ggc	aag	gag	ctg	cgc	aac	ggc	tcg	acg	gtg	gcg	ctg	gtg	tac	ctg	tcg
Gly	Lys	Glu	Leu	Arg	Asn	Gly	Ser	Thr	Val	Ala	Leu	Val	Tyr	Leu	Ser
	150					155					160				
ccg	gcc	gcc	aaa	ccc	gcc	gcg	acg	ggc	ctg	gag	tcg	acc	atg	cgg	ttc
Pro	Ala	Ala	Lys	Pro	Ala	Ala	Thr	Gly	Leu	Glu	Ser	Thr	Met	Arg	Phe
165					170					175					180
atc	ctg	tcg	gcc	aag	tcc	gcc	tac	gtc	gac	ggc	cag	gtc	ttc	tac	gtc
Ile	Leu	Ser	Ala	Lys	Ser	Ala	Tyr	Val	Asp	Gly	Gln	Val	Phe	Tyr	Val
				185					190					195	
ggc	gag	gcc	gac	tcc	acc	ccc	ccg	gcg	gac	tgg	gaa	cgg	ccg	ctg	gac
Gly	Glu	Ala	Asp	Ser	Thr	Pro	Pro	Ala	Asp	Trp	Glu	Arg	Pro	Leu	Asp
			200					205					210		
ggc	aag	gtc	gcc	atc	gtg	acc	ggt	gcg	gcc	cgc	gga	atc	ggc	gcc	acg
Gly	Lys	Val	Ala	Ile	Val	Thr	Gly	Ala	Ala	Arg	Gly	Ile	Gly	Ala	Thr
		215					220					225			
atc	gcc	gag	gtg	ttc	gcc	cgc	gac	ggc	gcc	cgc	gtg	gtc	gcg	atc	gac
Ile	Ala	Glu	Val	Phe	Ala	Arg	Asp	Gly	Ala	Arg	Val	Val	Ala	Ile	Asp
	230					235					240				
gtg	gaa	tcg	gcc	gcc	gag	acg	ctg	gcc	gag	acg	gcc	agc	cgg	gtc	ggc
Val	Glu	Ser	Ala	Ala	Glu	Thr	Leu	Ala	Glu	Thr	Ala	Ser	Arg	Val	Gly
245					250					255					260
ggc	acc	gcg	ctg	tgg	ctc	gac	gtc	acc	gcc	ccc	gac	gcc	gtc	gac	aag
Gly	Thr	Ala	Leu	Trp	Leu	Asp	Val	Thr	Ala	Pro	Asp	Ala	Val	Asp	Lys
				265					270					275	
atc	acc	gag	cac	ctg	cgc	gag	cac	cac	ggc	ggt	cac	gcc	gac	atc	ctg
Ile	Thr	Glu	His	Leu	Arg	Glu	His	His	Gly	Gly	His	Ala	Asp	Ile	Leu
			280					285					290		
gtc	aac	aac	gcc	ggg	atc	acc	cgc	gac	aag	ctg	ctg	gcc	aac	atg	gac
Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Lys	Leu	Leu	Ala	Asn	Met	Asp
		295					300					305			
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Asp	Ala	Arg	Trp	Asp	Ala	Val	Leu	Ala	Val	Asn	Leu	Leu	Ala	Pro	Leu
	310					315					320				
cgc	ctt	acc	gaa	ggg	ctg	gtg	ggc	aac	ggc	agc	atc	ggc	gaa	ggc	ggc
Arg	Leu	Thr	Glu	Gly	Leu	Val	Gly	Asn	Gly	Ser	Ile	Gly	Glu	Gly	Gly
325					330					335					340
cgc	atc	gtc	ggc	ctt	tcg	tcg	atg	gcc	ggc	atc	gcg	ggc	aac	cgc	ggc
Arg	Ile	Val	Gly	Leu	Ser	Ser	Met	Ala	Gly	Ile	Ala	Gly	Asn	Arg	Gly
				345					350					355	
cag	acc	aac	tac	gcc	acc	acc	aag	gca	ggc	atg	atc	ggc	ctc	acc	cag
Gln	Thr	Asn	Tyr	Ala	Thr	Thr	Lys	Ala	Gly	Met	Ile	Gly	Leu	Thr	Gln
			360					365					370		

Sequence 2002-032 US

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acc cgc gag gtg ggg cgc cgg atg aac tcg ctg ctg cag ggc ggg cag Thr Arg Glu Val Gly Arg Arg Met Asn Ser Leu Leu Gln Gly Gly Gln 405 410 415 420	1305
ccg gtg gac gtc gcc gaa acc atc gcc tac ttc gcc agc ccg gcg tcg Pro Val Asp Val Ala Glu Thr Ile Ala Tyr Phe Ala Ser Pro Ala Ser 425 430 435	1353
aac gcg gtg acc ggc aac gtc atc cgg gtc tgc ggc cag gcg atg ctg Asn Ala Val Thr Gly Asn Val Ile Arg Val Cys Gly Gln Ala Met Leu 440 445 450	1401
ggg gca tga Gly Ala	1410

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 <213> mycobacterium avium paratuberculosis

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Leu Ile Gly Gly Glu Gly Arg Val Val Glu Pro Leu Arg Ala Ala Leu 50 55 60
Ala Lys Asp Tyr Asp Leu Val Gly Asn Asn Leu Gly Gly Arg Trp Ala 65 70 75 80
Asp Arg Phe Gly Gly Leu Val Phe Asp Ala Thr Gly Ile Thr Thr Pro 85 90 95
Glu Gly Leu Lys Gly Leu Tyr Glu Phe Phe Thr Pro Leu Leu Arg Asn 100 105 110
Leu Gly His Cys Ala Arg Val Val Val Gly Thr Thr Pro Asp Ala 115 120 125

Sequence 2002-032 us

Ala Ala Gly Pro His Glu Arg Ile Ala Gln Arg Ala Leu Glu Gly Phe
130 135 140

Thr Arg Ser Leu Gly Lys Glu Leu Arg Asn Gly Ser Thr Val Ala Leu
145 150 155 160

Val Tyr Leu Ser Pro Ala Ala Lys Pro Ala Ala Thr Gly Leu Glu Ser
165 170 175

Thr Met Arg Phe Ile Leu Ser Ala Lys Ser Ala Tyr Val Asp Gly Gln
180 185 190

Val Phe Tyr Val Gly Glu Ala Asp Ser Thr Pro Pro Ala Asp Trp Glu
195 200 205

Arg Pro Leu Asp Gly Lys Val Ala Ile Val Thr Gly Ala Ala Arg Gly
210 215 220

Ile Gly Ala Thr Ile Ala Glu Val Phe Ala Arg Asp Gly Ala Arg Val
225 230 235 240

Val Ala Ile Asp Val Glu Ser Ala Ala Glu Thr Leu Ala Glu Thr Ala
245 250 255

Ser Arg Val Gly Gly Thr Ala Leu Trp Leu Asp Val Thr Ala Pro Asp
260 265 270

Ala Val Asp Lys Ile Thr Glu His Leu Arg Glu His His Gly Gly His
275 280 285

Ala Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Lys Leu Leu
290 295 300

Ala Asn Met Asp Asp Ala Arg Trp Asp Ala Val Leu Ala Val Asn Leu
305 310 315 320

Leu Ala Pro Leu Arg Leu Thr Glu Gly Leu Val Gly Asn Gly Ser Ile
325 330 335

Gly Glu Gly Gly Arg Ile Val Gly Leu Ser Ser Met Ala Gly Ile Ala
340 345 350

Gly Asn Arg Gly Gln Thr Asn Tyr Ala Thr Thr Lys Ala Gly Met Ile
355 360 365

Gly Leu Thr Gln Ala Leu Ala Pro Glu Leu Tyr Asp Lys Gly Ile Thr
370 375 380

Sequence 2002-032 US

Ile Asn Ala Val Ala Pro Gly Phe Ile Glu Thr Gln Met Thr Ala Ala
385 390 395 400

Ile Pro Leu Ala Thr Arg Glu Val Gly Arg Arg Met Asn Ser Leu Leu
405 410 415

Gln Gly Gly Gln Pro Val Asp Val Ala Glu Thr Ile Ala Tyr Phe Ala
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<223> n is a, c, g, or t

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gcaagtcgac gttcggcgcg aatcgggtgag gtgggcacag gtgaatgacg aagaggac 178
atg ctg gtc gcc acg gtg cgg gcg ttc atc gac cgc gag gtc aaa ccg 226
Met Leu Val Ala Thr Val Arg Ala Phe Ile Asp Arg Glu Val Lys Pro
1 5 10 15
acc gtg cgc gag gtg gag cac gcc gat gcc tat ccc gag gcg tgg atc 274
Thr Val Arg Glu Val Glu His Ala Asp Ala Tyr Pro Glu Ala Trp Ile
20 25 30
gag cag atg aag cgg atc ggg atc tac ggg ctg gcg gtg ccc gag gaa 322
Glu Gln Met Lys Arg Ile Gly Ile Tyr Gly Leu Ala Val Pro Glu Glu
35 40 45
tac ggt ggt tcg ccg gtg tcc atg ccg tgc tac gtg cgg gtc acc gag 370
Tyr Gly Gly Ser Pro Val Ser Met Pro Cys Tyr Val Arg Val Thr Glu

Sequence 2002-032 US
60

50	55	60	
cag ctg gcg cgc ggc tgg atg agc ctg gcc ggg gcg atg ggc ggg cac Gln Leu Ala Arg Gly Trp Met Ser Leu Ala Gly Ala Met Gly Gly His 65 70 75 80			418
acc gtg gtg gcc aag ctg cta acg ctg ttc ggc acc gag gac cas aag Thr Val Val Ala Lys Leu Leu Thr Leu Phe Gly Thr Glu Asp Xaa Lys 85 90 95			466
cgg gcc tac ctg ccg cgg atg gcc agc ggc gaa atc cgg gcc acc atg Arg Ala Tyr Leu Pro Arg Met Ala Ser Gly Glu Ile Arg Ala Thr Met 100 105 110			514
gcg ttg acc gag ccc sgc ggc ggc tcg gac ctg cag aac atg tcg acc Ala Leu Thr Glu Pro Xaa Gly Gly Ser Asp Leu Gln Asn Met Ser Thr 115 120 125			562
acc gcg ctg ccc gac ccc gac tcc gac ggn ctg gtg gtc aac ggg gcc Thr Ala Leu Pro Asp Pro Asp Ser Asp Gly Leu Val Val Asn Gly Ala 130 135 140			610
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<223> The 'Xaa' at location 95 stands for Gln, or His.

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Glu Gln Met Lys Arg Ile Gly Ile Tyr Gly Leu Ala Val Pro Glu Glu
35 40 45

Tyr Gly Gly Ser Pro Val Ser Met Pro Cys Tyr Val Arg Val Thr Glu
50 55 60

Sequence 2002-032 US

Gln Leu Ala Arg Gly Trp Met Ser Leu Ala Gly Ala Met Gly Gly His
65 70 75 80

Thr Val Val Ala Lys Leu Leu Thr Leu Phe Gly Thr Glu Asp Xaa Lys
85 90 95

Arg Ala Tyr Leu Pro Arg Met Ala Ser Gly Glu Ile Arg Ala Thr Met
100 105 110

Ala Leu Thr Glu Pro Xaa Gly Gly Ser Asp Leu Gln Asn Met Ser Thr
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Lys Thr Xaa Ile Asn
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cgaaacggac cggaggtgaa agggac atg agc cac gcc gat caa ctc gct cgg 173
Met Ser His Ala Asp Gln Leu Ala Arg
1 5
acg cac ctg gcg ccc gat cct gcg gac ctg tcg cgc ctg gtc gcc gcc 221
Thr His Leu Ala Pro Asp Pro Ala Asp Leu Ser Arg Leu Val Ala Gly
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Thr His His Asp Pro His
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1 5 10 15

Sequence 2002-032 US

Ala Asp Leu Ser Arg Leu Val Ala Gly Thr His His Asp Pro His
20 25 30

<210> 13
<211> 236
<212> DNA
<213> mycobacterium avium paratuberculosis

<220>
<221> CDS
<222> (8)..(214)

<400> 13
ggacacc aac gtg acc ggg gtg ttt ctc acc gcc cag gcg gcg gcc cgg 49
1 Asn Val Thr Gly Val Phe Leu Thr Ala Gln Ala Ala Ala Arg
15 gcg atg atg cgg cag ggc cgc ggc ggc gcc atc atc acc acc gcc tcg 97
Ala Met Met Arg Gln Gly Arg Gly Gly Ala Ile Ile Thr Thr Ala Ser
20 25 30
atg tcc ggg cac atc atc aac gtc ccg cag cag gtc ggc cac tac tgc 145
Met Ser Gly His Ile Ile Asn Val Pro Gln Gln Val Gly His Tyr Cys
35 40 45
gcc agc aag gcg gcc gtg atc cag ctg acc aag gcc atg gcc gtc gaa 193
Ala Ser Lys Ala Ala Val Ile Gln Leu Thr Lys Ala Met Ala Val Glu
50 55 60
ttc tgc agg atc cgt cga ctc tagactcgag caagcttatg ca 236
Phe Cys Arg Ile Arg Arg Leu
65

<210> 14
<211> 69
<212> PRT
<213> mycobacterium avium paratuberculosis

<400> 14
Asn Val Thr Gly Val Phe Leu Thr Ala Gln Ala Ala Ala Arg Ala Met
1 5 10 15
Met Arg Gln Gly Arg Gly Gly Ala Ile Ile Thr Thr Ala Ser Met Ser
20 25 30
Gly His Ile Ile Asn Val Pro Gln Gln Val Gly His Tyr Cys Ala Ser
35 40 45
Lys Ala Ala Val Ile Gln Leu Thr Lys Ala Met Ala Val Glu Phe Cys
50 55 60
Arg Ile Arg Arg Leu
65

Sequence 2002-032 us

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<210> 15
<211> 419
<212> DNA
<213> mycobacterium avium paratuberculosis
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<220>
<221> CDS
<222> (25) .. (417)

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<220>
<221> misc_feature
<222> (331)..(331)
<223> n is a, c, g, or t
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<220>
<221> misc_feature
<222> (398)..(398)
<223> n is a, c, g, or t
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<400> 15
cggccaccgc acccagggga ggcc atg act cac acc aag gcc ggt cgt gcc 51
Met Thr His Thr Lys Ala Gly Arg Ala
1 5

gcg tgg ccg gcc gcc tgc gcg gtc gtc ctg tcc gcc gcc gcg ctg ttg 99
Ala Trp Pro Ala Ala Cys Ala Val Val Leu Ser Ala Ala Ala Leu Leu
10 15 20 25

tgc gcg gca gcg gcc gcc gcg gac gaa gcc gat gac gcg ttc ctc gcc 147
Cys Ala Ala Ala Ala Ala Ala Asp Glu Ala Asp Asp Ala Phe Leu Ala
30 35 40

ggc ctg gcc aag ggc ggg atc acc atg ttc gac gac gac gac gcg atc 195
Gly Leu Ala Lys Gly Gly Ile Thr Met Phe Asp Asp Asp Asp Ala Ile
45 50 55

gcc atg ggc cac agc gtg tgc tgc agc atc gac gcc aac ccc aac gtg 243
Ala Met Gly His Ser Val Cys Ser Ser Ile Asp Ala Asn Pro Asn Val
60 65 70

tcg atg ctg gcg ctg cgg ctg acc aag caa acc ccg ttg acg ccg aag 291
Ser Met Leu Ala Leu Arg Leu Thr Lys Gln Thr Pro Leu Thr Pro Lys
75 80 85

caa tcc ggc tac ttc atc ggt ctt tcg gtc gcc agc tac ntg ccc gca 339
Gln Ser Gly Tyr Phe Ile Gly Leu Ser Val Ala Ser Tyr Xaa Pro Ala
90 95 100 105

gta caa gga cga cgt cga ccc ctc gct ggg ctg gct gat ccc gcc gcc 387
Val Gln Gly Arg Arg Arg Pro Leu Ala Gly Leu Ala Asp Pro Ala Ala
110 115 120

gct gat gtg ang ttg ccg gcc ggc atc ggc gt 419
Ala Asp Val Xaa Leu Pro Ala Gly Ile Gly
125 130

<210>	16
<211>	131
<212>	PRT

Sequence 2002-032 US

<213> mycobacterium avium paratuberculosis

<220>

<221> misc_feature

<222> (103)..(103)

<223> The 'xaa' at location 103 stands for Met, Val, or Leu.

<220>

<221> misc_feature

<222> (125)..(125)

<223> The 'xaa' at location 125 stands for Lys, Arg, Thr, or Met.

<400> 16

Met Thr His Thr Lys Ala Gly Arg Ala Ala Trp Pro Ala Ala Cys Ala
1 5 10 15

Val Val Leu Ser Ala Ala Ala Leu Leu Cys Ala Ala Ala Ala Ala Ala
20 25 30

Asp Glu Ala Asp Asp Ala Phe Leu Ala Gly Leu Ala Lys Gly Gly Ile
35 40 45

Thr Met Phe Asp Asp Asp Asp Ala Ile Ala Met Gly His Ser Val Cys
50 55 60

Ser Ser Ile Asp Ala Asn Pro Asn Val Ser Met Leu Ala Leu Arg Leu
65 70 75 80

Thr Lys Gln Thr Pro Leu Thr Pro Lys Gln Ser Gly Tyr Phe Ile Gly
85 90 95

Leu Ser Val Ala Ser Tyr Xaa Pro Ala Val Gln Gly Arg Arg Arg Pro
100 105 110

Leu Ala Gly Leu Ala Asp Pro Ala Ala Ala Asp Val Xaa Leu Pro Ala
115 120 125

Gly Ile Gly
130

<210> 17

<211> 392

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (94)..(390)

<400> 17

cggcgtagca tcgtcaagtc gttgcccgcg ctgatgccgg agcggcagta aggagttcgg

60

Sequence 2002-032 US

ctggtgcaaa aacgcttgcc cacagtcggtt ttg gtg ctg acg gcc gtt gtc gcc 114
Val Leu Thr Ala Val Val Ala
1 5

ggt atc gcc ggg tgc agc gcg gcg cag acc gtg ccg cgc aag gcc gcc 162
Gly Ile Ala Gly Cys Ser Ala Ala Gln Thr Val Pro Arg Lys Ala Ala
10 15 20

cgg ctg acc atc gac ggt gcc acc cac acg acc cgc ccg ccg tcc tgc 210
Arg Leu Thr Ile Asp Gly Ala Thr His Thr Thr Arg Pro Pro Ser Cys
25 30 35

cgg cag gac cag atg tat cgg acc atc aac atc ccc gac cac gac ggt 258
Arg Gln Asp Gln Met Tyr Arg Thr Ile Asn Ile Pro Asp His Asp Gly
40 45 50 55

gga gtc gaa gcg gtg gtg ctg ctc agc ggt tac cgg gtg atg ccg cag 306
Gly Val Glu Ala Val Val Leu Leu Ser Gly Tyr Arg Val Met Pro Gln
60 65 70

tgg gtg aag atc cgg aac gtc gac ggc ttc acc ggc agt cta ctg gcc 354
Trp Val Lys Ile Arg Asn Val Asp Gly Phe Thr Gly Ser Leu Leu Ala
75 80 85

asg gcg gag tgg gcg acg cgc acg tcg atc tca cma at 392
Xaa Ala Glu Trp Ala Thr Arg Thr Ser Ile Ser Xaa
90 95

<210> 18
<211> 99
<212> PRT
<213> mycobacterium avium paratuberculosis

<220>
<221> misc_feature
<222> (88)..(88)
<223> The 'xaa' at location 88 stands for Arg, or Thr.

<220>
<221> misc_feature
<222> (99)..(99)
<223> The 'xaa' at location 99 stands for Gln, or Pro.

<400> 18

Val Leu Thr Ala Val Val Ala Gly Ile Ala Gly Cys Ser Ala Ala Gln
1 5 10 15

Thr Val Pro Arg Lys Ala Ala Arg Leu Thr Ile Asp Gly Ala Thr His
20 25 30

Thr Thr Arg Pro Pro Ser Cys Arg Gln Asp Gln Met Tyr Arg Thr Ile
35 40 45

Asn Ile Pro Asp His Asp Gly Gly Val Glu Ala Val Val Leu Leu Ser
50 55 60

Gly Tyr Arg Val Met Pro Gln Trp Val Lys Ile Arg Asn Val Asp Gly
Page 17

Sequence 2002-032 US

65

70

75

80

Phe Thr Gly Ser Leu Leu Ala Xaa Ala Glu Trp Ala Thr Arg Thr Ser
85 90 95

Ile Ser Xaa

<210> 19

<211> 1884

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (13)..(1884)

<400> 19

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Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn
1 5 10

tcc gtc gtc gca gtc ctc gag ggc ggt gac ccc gtc gtc gtc gcc aac 99
Ser Val Val Ala Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn
15 20 25

tcc gag ggc tcg cgg acc acc ccg tcc atc gtc gcg ttc gcc cgc aac 147
Ser Glu Gly Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn
30 35 40 45

ggc gag gtg ctc gtc ggc cag ccc gcc aag aac cag gcg gtg acc aac 195
Gly Glu Val Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn
50 55 60

gtc gac cgc acc atc cgt tcg gtc aag cgg cac atg ggc acc gac tgg 243
Val Asp Arg Thr Ile Arg Ser Val Lys Arg His Met Gly Thr Asp Trp
65 70 75

tcc atc gag atc gac ggc aag aaa tac acc gct cag gag atc agc gcc 291
Ser Ile Glu Ile Asp Gly Lys Lys Tyr Thr Ala Gln Glu Ile Ser Ala
80 85 90

cgc gtg ctg atg aag ctc aag cgc gac gcc gag gcc tat ctg ggt gag 339
Arg Val Leu Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu
95 100 105

gac atc acc gac gcg gtc atc acc gta ccg gcg tac ttc aac gac gcc 387
Asp Ile Thr Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala
110 115 120 125

cag cgt cag gcg acc aag gaa gcc ggc cag atc gcc ggc ctc aac gtg 435
Gln Arg Gln Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val
130 135 140

ctg cgc atc gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctg 483
Leu Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu
145 150 155

gac aag ggc gag aag gag cag acc atc ctg gtc ttc gac ctc ggc ggc 531

Sequence 2002-032 US																
Asp	Lys	Gly	Glu	Lys	Glu	Gln	Thr	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	
		160					165					170				
ggc	acg	ttc	gac	gtt	tcg	ctg	ctc	gag	atc	ggc	gag	ggt	gtg	gtc	gag	579
Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Glu	Gly	Val	Val	Glu	
	175					180					185					
gtc	cgc	gcc	acc	agc	ggt	gac	aac	caa	ctc	ggt	ggc	gac	gac	tgg	gac	627
Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	Gln	Leu	Gly	Gly	Asp	Asp	Trp	Asp	
190					195					200					205	
gac	cgg	atc	gtc	aac	tgg	ctg	gtc	gac	aag	ttc	aag	ggc	acc	agc	ggc	675
Asp	Arg	Ile	Val	Asn	Trp	Leu	Val	Asp	Lys	Phe	Lys	Gly	Thr	Ser	Gly	
				210					215					220		
atc	gac	ctg	acc	aag	gac	aag	atg	gcc	atg	cag	cgg	ctg	cgt	gag	gcc	723
Ile	Asp	Leu	Thr	Lys	Asp	Lys	Met	Ala	Met	Gln	Arg	Leu	Arg	Glu	Ala	
			225					230					235			
gcc	gag	aag	gcc	aag	atc	gag	ttg	tcc	agc	tcg	cag	agc	acc	tcg	atc	771
Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Thr	Ser	Ile	
		240					245					250				
aac	ctg	ccc	tac	atc	acc	gtc	gac	gcg	gac	aag	aac	ccg	ctg	ttc	ctc	819
Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	
	255					260					265					
gac	gag	cag	ctg	acc	cgc	gcc	gaa	ttc	cag	cgc	atc	acc	cag	gat	ctg	867
Asp	Glu	Gln	Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	
270					275					280					285	
ctg	gac	cgc	acc	cgt	cag	ccg	ttc	aag	tcg	gtg	atc	gcc	gac	gcc	ggc	915
Leu	Asp	Arg	Thr	Arg	Gln	Pro	Phe	Lys	Ser	Val	Ile	Ala	Asp	Ala	Gly	
				290					295					300		
atc	tcg	gtg	tcc	gac	atc	gac	cac	gtg	gtg	ctg	gtg	ggt	ggt	tcc	acc	963
Ile	Ser	Val	Ser	Asp	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	
			305					310					315			
cgg	atg	ccc	gcg	gtg	acc	gac	ctg	gtc	aag	gaa	ctc	acc	ggc	ggc	aag	1011
Arg	Met	Pro	Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	
		320					325					330				
gag	ccc	aac	aag	ggc	gtc	aac	ccc	gac	gag	gtt	gtc	gcg	gtg	ggt	gcc	1059
Glu	Pro	Asn	Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	
	335					340					345					
gcc	ctg	cag	gcc	ggt	gtg	ctt	aag	ggc	gag	gtg	aaa	gac	gtt	ctg	ctg	1107
Ala	Leu	Gln	Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	
350				355						360					365	
ctt	gac	gtt	acg	ccg	ctg	agc	ctg	ggt	atc	gag	acc	aag	ggt	ggc	gtg	1155
Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	
				370				375						380		
atg	acc	aag	ctg	atc	gaa	cgc	aac	acc	acc	atc	ccg	acc	aag	cgg	tcc	1203
Met	Thr	Lys	Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	
			385					390					395			
gag	acg	ttc	acc	acg	gcc	gac	gac	aac	cag	ccg	tcg	gtg	cag	atc	cag	1251
Glu	Thr	Phe	Thr	Thr	Ala	Asp	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	
		400					405					410				

Sequence 2002-032 US																
gtg	tat	cag	ggt	gag	cgc	gaa	atc	gcc	gcg	cac	aac	aag	ctg	ctc	ggc	1299
Val	Tyr	Gln	Gly	Glu	Arg	Glu	Ile	Ala	Ala	His	Asn	Lys	Leu	Leu	Gly	
	415					420					425					
tcc	ttc	gag	ctg	acc	gga	att	ccg	ccg	gcg	ccc	cgc	ggc	gtg	ccg	cag	1347
Ser	Phe	Glu	Leu	Thr	Gly	Ile	Pro	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	
	430				435					440					445	
atc	gag	gtc	acc	ttc	gac	atc	gac	gcc	aac	ggc	atc	gtg	cac	gtc	acc	1395
Ile	Glu	Val	Thr	Phe	Asp	Ile	Asp	Ala	Asn	Gly	Ile	Val	His	Val	Thr	
				450					455					460		
gcc	aag	gac	aag	ggc	acc	ggt	aag	gag	aac	acg	atc	aag	atc	cag	gag	1443
Ala	Lys	Asp	Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Lys	Ile	Gln	Glu	
			465					470					475			
ggc	tcc	ggc	ctg	tcc	aag	gag	gag	atc	gac	cgg	atg	atc	aag	gac	gcc	1491
Gly	Ser	Gly	Leu	Ser	Lys	Glu	Glu	Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	
		480				485						490				
gag	gcg	cac	gcc	gag	gag	gac	cgc	aag	agg	cgc	gag	gaa	gcc	gac	gtc	1539
Glu	Ala	His	Ala	Glu	Glu	Asp	Arg	Lys	Arg	Arg	Glu	Glu	Ala	Asp	Val	
	495					500					505					
cgc	aac	caa	gcg	gaa	tcg	ctt	gtc	tac	cag	acg	gag	aag	ttc	gtc	aag	1587
Arg	Asn	Gln	Ala	Glu	Ser	Leu	Val	Tyr	Gln	Thr	Glu	Lys	Phe	Val	Lys	
	510				515					520					525	
gac	cag	cgc	gag	gcc	gag	ggc	ggc	tcg	aag	gtt	ccc	gag	gag	acg	ctg	1635
Asp	Gln	Arg	Glu	Ala	Glu	Gly	Gly	Ser	Lys	Val	Pro	Glu	Glu	Thr	Leu	
				530					535					540		
tcc	aag	gtc	gac	gcc	gcg	atc	gcc	gac	gcc	aag	acg	gcc	ctg	ggc	ggc	1683
Ser	Lys	Val	Asp	Ala	Ala	Ile	Ala	Asp	Ala	Lys	Thr	Ala	Leu	Gly	Gly	
			545					550					555			
acc	gac	atc	acc	gcg	atc	aag	tcg	gcg	atg	gag	aag	ctc	ggc	cag	gag	1731
Thr	Asp	Ile	Thr	Ala	Ile	Lys	Ser	Ala	Met	Glu	Lys	Leu	Gly	Gln	Glu	
		560					565					570				
tcg	caa	gcg	ctg	gga	cag	gca	atc	tac	gag	gcc	acc	cag	gcc	gag	tcc	1779
Ser	Gln	Ala	Leu	Gly	Gln	Ala	Ile	Tyr	Glu	Ala	Thr	Gln	Ala	Glu	Ser	
	575					580					585					
gcc	cag	gct	ggc	ggg	ccg	gac	ggt	gcc	gcg	gcc	ggc	ggc	ggg	tcc	gga	1827
Ala	Gln	Ala	Gly	Gly	Pro	Asp	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Ser	Gly	
	590				595					600					605	
tcc	gcc	gac	gat	gtt	gtg	gac	gcg	gag	gtg	gtc	gac	gat	gac	cgg	gag	1875
Ser	Ala	Asp	Asp	Val	Val	Asp	Ala	Glu	Val	Val	Asp	Asp	Asp	Arg	Glu	
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tcc	aag	tga														1884
Ser	Lys															

<210> 20
 <211> 623
 <212> PRT
 <213> mycobacterium avium paratuberculosis

<400> 20

Sequence 2002-032 US

Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
1 5 10 15
Ala Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
20 25 30
Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
35 40 45
Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
50 55 60
Thr Ile Arg Ser Val Lys Arg His Met Gly Thr Asp Trp Ser Ile Glu
65 70 75 80
Ile Asp Gly Lys Lys Tyr Thr Ala Gln Glu Ile Ser Ala Arg Val Leu
85 90 95
Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
100 105 110
Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
115 120 125
Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
130 135 140
Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
145 150 155 160
Glu Lys Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
165 170 175
Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
180 185 190
Thr Ser Gly Asp Asn Gln Leu Gly Gly Asp Asp Trp Asp Asp Arg Ile
195 200 205
Val Asn Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile Asp Leu
210 215 220
Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
225 230 235 240
Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
245 250 255

Sequence 2002-032 US

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 260 265 270
 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
 275 280 285
 Thr Arg Gln Pro Phe Lys Ser Val Ile Ala Asp Ala Gly Ile Ser Val
 290 295 300
 Ser Asp Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
 405 410 415
 Gly Glu Arg Glu Ile Ala Ala His Asn Lys Leu Leu Gly Ser Phe Glu
 420 425 430
 Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
 435 440 445
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
 450 455 460
 Lys Gly Thr Gly Lys Glu Asn Thr Ile Lys Ile Gln Glu Gly Ser Gly
 465 470 475 480
 Leu Ser Lys Glu Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
 485 490 495
 Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val Arg Asn Gln
 Page 22

Sequence 2002-032 US

500

505

510

Ala Glu Ser Leu Val Tyr Gln Thr Glu Lys Phe Val Lys Asp Gln Arg
515 520 525

Glu Ala Glu Gly Gly Ser Lys Val Pro Glu Glu Thr Leu Ser Lys Val
530 535 540

Asp Ala Ala Ile Ala Asp Ala Lys Thr Ala Leu Gly Gly Thr Asp Ile
545 550 555 560

Thr Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser Gln Ala
565 570 575

Leu Gly Gln Ala Ile Tyr Glu Ala Thr Gln Ala Glu Ser Ala Gln Ala
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Gly Gly Pro Asp Gly Ala Ala Ala Gly Gly Gly Ser Gly Ser Ala Asp
595 600 605

Asp Val Val Asp Ala Glu Val Val Asp Asp Asp Arg Glu Ser Lys
610 615 620

<210> 21
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<220>
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Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg
1 5 10
cgc ggc ctc gag cgg ggg ctc aac gcc ctc gcc gac gcg gta aag gtc 159
Arg Gly Leu Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val
15 20 25
acg ttg ggc ccc aag ggt cgc aac gtc gtc ctg gag aag aag tgg ggt 207
Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly
30 35 40
gcc ccc acg atc acc aac gat ggt gtg tcc atc gcc aag gag atc gag 255
Ala Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
45 50 55 60
ctg gag gac ccg tac gag aag atc ggc gcc gag ctg gtc aag gaa gtc 303
Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val
65 70 75

Sequence 2002-032 US

gcc Ala	aag Lys	aag Lys	acc Thr 80	gac Asp	gac Asp	gtc Val	gcc Ala	ggt Gly 85	gac Asp	ggc Gly	acg Thr	acg Thr	acg Thr 90	gcc Ala	acg Thr	351
gtg Val	ctc Leu	gcc Ala 95	cag Gln	gcg Ala	ttg Leu	gtc Val	cgc Arg 100	gag Glu	ggc Gly	ctg Leu	cgc Arg	aac Asn 105	gtc Val	gcg Ala	gcc Ala	399
ggc Gly	gcc Ala 110	aac Asn	ccg Pro	ctg Leu	ggt Gly	ctc Leu 115	aag Lys	cgc Arg	ggc Gly	atc Ile	gag Glu 120	aag Lys	gcc Ala	gtc Val	gag Glu	447
aag Lys 125	gtc Val	acc Thr	gag Glu	acc Thr	ctg Leu 130	ctc Leu	aag Lys	tcg Ser	gcc Ala	aag Lys 135	gag Glu	gtc Val	gag Glu	acc Thr	aag Lys 140	495
gac Asp	cag Gln	atc Ile	gct Ala	gcc Ala 145	acc Thr	gcg Ala	gcc Ala	atc Ile	tcc Ser 150	gcg Ala	ggc Gly	gac Asp	cag Gln	tcg Ser 155	atc Ile	543
ggc Gly	gac Asp	ctg Leu	atc Ile 160	gcc Ala	gag Glu	gcg Ala	atg Met	gac Asp 165	aag Lys	gtc Val	ggc Gly	aac Asn	gag Glu 170	ggc Gly	gtc Val	591
atc Ile	acc Thr	gtc Val 175	gag Glu	gag Glu	tcc Ser	aac Asn	acc Thr 180	ttc Phe	ggc Gly	ctg Leu	cag Gln	ctc Leu 185	gag Glu	ctc Leu	acc Thr	639
gag Glu	ggt Gly 190	atg Met	cgg Arg	ttc Phe	gac Asp	aag Lys 195	ggt Gly	tac Tyr	atc Ile	tcg Ser	ggc Gly 200	tac Tyr	ttc Phe	gtc Val	acg Thr	687
gac Asp 205	gcc Ala	gag Glu	cgt Arg	cag Gln	gaa Glu 210	gcg Ala	gtc Val	ctc Leu	gag Glu	gac Asp 215	ccg Pro	ttc Phe	atc Ile	ctg Leu	ctg Leu 220	735
gtc Val	agc Ser	tcc Ser	aag Lys	gtc Val 225	tcg Ser	acc Thr	gtc Val	aag Lys	gac Asp 230	ctg Leu	ctg Leu	ccg Pro	ctg Leu	ctg Leu 235	gag Glu	783
aag Lys	gtc Val	atc Ile	cag Gln 240	gcc Ala	ggc Gly	aag Lys	ccg Pro	ctg Leu 245	ctg Leu	atc Ile	atc Ile	gcc Ala	gag Glu 250	gac Asp	gtc Val	831
gag Glu	ggc Gly	gag Glu 255	gcc Ala	ctg Leu	tcc Ser	acc Thr	ctg Leu 260	gtc Val	gtc Val	aac Asn	aag Lys	atc Ile 265	cgc Arg	ggc Gly	acc Thr	879
ttc Phe	aag Lys 270	tcg Ser	gtg Val	gcc Ala	gtc Val	aag Lys 275	gcg Ala	ccc Pro	ggc Gly	ttc Phe	ggc Gly 280	gac Asp	cgc Arg	cgc Arg	aag Lys	927
gcg Ala 285	atg Met	ctt Leu	cag Gln	gac Asp	atg Met 290	gcc Ala	atc Ile	ctc Leu	acc Thr	ggc Gly 295	ggc Gly	cag Gln	gtc Val	atc Ile	agc Ser 300	975
gaa Glu	gag Glu	gtc Val	ggc Gly 305	ctg Leu	tcg Ser	ctg Leu	gag Glu	agc Ser	gcc Ala 310	gac Asp	atc Ile	tcg Ser	ctg Leu	ctc Leu 315	ggt Gly	1023
aag Lys	gcc Ala	cgc Arg	aag Lys	gtc Val	gtc Val	gtc Val	acc Thr	aag Lys	gac Asp	gag Glu	acc Thr	acc Thr	atc Ile	gtc Val	gag Glu	1071

Sequence 2002-032 US																
320				325				330								
ggc	gcc	ggt	gac	tcc	gac	gcc	atc	gcc	ggc	cgg	gtg	gcc	cag	atc	cgc	1119
Gly	Ala	Gly	Asp	Ser	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg	
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acc	gag	atc	gag	aac	agc	gac	tcc	gac	tac	gac	cgc	gag	aag	ctg	cag	1167
Thr	Glu	Ile	Glu	Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	
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gag	cgg	ctg	gcc	aag	ctg	gcc	ggc	ggc	gtg	gcg	gtg	atc	aag	gcc	ggc	1215
Glu	Arg	Leu	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Ala	Gly	
365					370					375					380	
gcc	gcg	acc	gag	gtc	gag	ctc	aag	gag	cgc	aag	cac	cgc	atc	gag	gac	1263
Ala	Ala	Thr	Glu	Val	Glu	Leu	Lys	Glu	Arg	Lys	His	Arg	Ile	Glu	Asp	
				385					390					395		
gcg	gtc	cgc	aac	gcc	aag	gcg	gcc	gtg	gag	gag	ggc	atc	gtc	gcc	ggc	1311
Ala	Val	Arg	Asn	Ala	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	
			400					405					410			
ggt	ggc	gtg	gcc	ctg	ctg	cac	gcg	atc	ccg	gct	ctg	gac	gag	ctg	aag	1359
Gly	Gly	Val	Ala	Leu	Leu	His	Ala	Ile	Pro	Ala	Leu	Asp	Glu	Leu	Lys	
		415					420					425				
ctc	gag	ggc	gaa	gag	gcg	acc	ggc	gcc	aac	atc	gtc	cgg	gtg	gcc	ctc	1407
Leu	Glu	Gly	Glu	Glu	Ala	Thr	Gly	Ala	Asn	Ile	Val	Arg	Val	Ala	Leu	
	430					435					440					
gag	gct	ccg	ctg	aag	cag	atc	gcc	ttc	aac	ggt	ggc	ctg	gag	ccc	ggc	1455
Glu	Ala	Pro	Leu	Lys	Gln	Ile	Ala	Phe	Asn	Gly	Gly	Leu	Glu	Pro	Gly	
445					450					455					460	
gtg	gtg	gcc	gag	aag	gtc	gcg	aac	tcg	ccc	gcc	ggt	acc	ggc	ctc	aac	1503
Val	Val	Ala	Glu	Lys	Val	Arg	Asn	Ser	Pro	Ala	Gly	Thr	Gly	Leu	Asn	
				465					470					475		
gcc	gcc	acc	ggt	gag	tac	gag	gac	ctg	ctc	aag	gcc	ggc	att	gcc	gac	1551
Ala	Ala	Thr	Gly	Glu	Tyr	Glu	Asp	Leu	Leu	Lys	Ala	Gly	Ile	Ala	Asp	
			480					485					490			
ccg	gtg	aag	gtc	acc	gcg	tcg	gcg	ctg	cag	aac	gcg	gcg	tcc	atc	gcg	1599
Pro	Val	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	
		495					500					505				
ggg	ctg	ttc	ctg	acc	acc	gag	gcg	gtc	gtc	gcc	gac	aag	ccg	gag	aag	1647
Gly	Leu	Phe	Leu	Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	
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gcg	gcc	gct	ccc	gcg	ggc	gac	ccg	acc	ggc	ggc	atg	ggc	ggc	atg	gac	1695
Ala	Ala	Ala	Pro	Ala	Gly	Asp	Pro	Thr	Gly	Gly	Met	Gly	Gly	Met	Asp	
525					530					535					540	
ttc	tga															1701
Phe																

<210> 22
 <211> 541
 <212> PRT
 <213> mycobacterium avium paratuberculosis

Sequence 2002-032 US

<400> 22

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Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
35     40     45
Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
50     55     60
Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
65     70     75     80
Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
85     90     95
Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
100    105    110
Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu
115    120    125
Thr Leu Leu Lys Ser Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala
130    135    140
Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
145    150    155    160
Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
165    170    175
Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
180    185    190
Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
195    200    205
Gln Glu Ala Val Leu Glu Asp Pro Phe Ile Leu Leu Val Ser Ser Lys
210    215    220
Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
225    230    235    240

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Sequence 2002-032 US

Ala Gly Lys Pro Leu₂₄₅ Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala₂₅₅
 Leu Ser Thr Leu₂₆₀ Val Val Asn Lys Ile₂₆₅ Arg Gly Thr Phe Lys₂₇₀ Ser Val
 Ala Val Lys₂₇₅ Ala Pro Gly Phe Gly₂₈₀ Asp Arg Arg Lys Ala₂₈₅ Met Leu Gln
 Asp Met₂₉₀ Ala Ile Leu Thr Gly₂₉₅ Gly Gln Val Ile Ser₃₀₀ Glu Glu Val Gly
 Leu Ser₃₀₅ Leu Glu Ser Ala₃₁₀ Asp Ile Ser Leu Leu₃₁₅ Gly Lys Ala Arg Lys₃₂₀
 Val Val Val Thr Lys₃₂₅ Asp Glu Thr Thr Ile₃₃₀ Val Glu Gly Ala Gly₃₃₅ Asp
 Ser Asp Ala Ile₃₄₀ Ala Gly Arg Val Ala₃₄₅ Gln Ile Arg Thr Glu₃₅₀ Ile Glu
 Asn Ser Asp₃₅₅ Ser Asp Tyr Asp Arg₃₆₀ Glu Lys Leu Gln Glu₃₆₅ Arg Leu Ala
 Lys Leu₃₇₀ Ala Gly Gly Val Ala₃₇₅ Val Ile Lys Ala Gly₃₈₀ Ala Ala Thr Glu
 Val₃₈₅ Glu Leu Lys Glu Arg₃₉₀ Lys His Arg Ile Glu₃₉₅ Asp Ala Val Arg Asn₄₀₀
 Ala Lys Ala Ala Val₄₀₅ Glu Glu Gly Ile Val₄₁₀ Ala Gly Gly Gly Val₄₁₅ Ala
 Leu Leu His Ala₄₂₀ Ile Pro Ala Leu Asp₄₂₅ Glu Leu Lys Leu Glu₄₃₀ Gly Glu
 Glu Ala Thr₄₃₅ Gly Ala Asn Ile Val₄₄₀ Arg Val Ala Leu Glu₄₄₅ Ala Pro Leu
 Lys Gln Ile Ala Phe Asn Gly₄₅₅ Gly Leu Glu Pro Gly₄₆₀ Val Val Ala Glu
 Lys Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly₄₈₀
 Glu Tyr Glu Asp Leu₄₈₅ Leu Lys Ala Gly Ile₄₉₀ Ala Asp Pro Val Lys₄₉₅ Val

Sequence 2002-032 US

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
500 505 510

Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Ala Ala Pro
515 520 525

Ala Gly Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe
530 535 540